Eric Christopher Anderson

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Born January 25, 1970
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EDUCATION

Ph.D. (Quant. Ecol. & Res. Mgmt.)	2001	University of Washington, Seattle, WA
M.S. (Fisheries)	1998	University of Washington, Seattle, WA
B.A. (Human Biology)	1993	Stanford University, Stanford, CA
—	1990–91	Prescott College, Prescott, AZ
High School Diploma	1988	The Thacher School, Ojai, CA

GRANTS AND FELLOWSHIPS

1999–01 Designated Research Assistant, National Science Foundation Grant #BIR-9807747, "Computational Methods for Inference of Population Parameters," (PI: E.A. Thompson).

1996–99 Trainee, National Science Foundation Mathematical Biology Training Grant #BIR-9256532, University of Washington. (PIs: G.M Odell and T.L. Daniel)

1998 Fellow, Program in Mathematics and Molecular Biology, Burroughs Wellcome Fund, University of Washington.

1994–96 Fellow, H. Mason Keeler Endowment for Excellence. School of Fisheries, University of Washington.

HONORS AND AWARDS

2000 First Prize, Western North American Region Student Papers Competition, International Biometrics Society Conference, July, 2000, Berkeley, CA, for talk titled "Bayesian analysis of genetic mixture and admixture."

1993 Phi Beta Kappa and graduation "With Distinction," Stanford University.

EMPLOYMENT

2003– Research Molecular Geneticist, National Marine Fisheries Service, Southwest Fisheries Science Center, Santa Cruz Lab, Santa Cruz, California.

2001–03 Postdoctoral Researcher, National Institutes of Health Grant #GM-40282 to Montgomery Slatkin, "Models of Complex Genetic Systems." Department of Integrative Biology, University of California, Berkeley.

1999–01 Research Assistant, NSF Grant #BIR-9807747 to Elizabeth A. Thompson, "Computational Methods for Inference of Population Parameters." Department of Statistics, University of Washington, Seattle.

1999 Pre-Doctoral Lecturer. Prepared syllabus and lectured for the first four weeks of Biology 472, Advanced Undergraduate Ecology. Summer. University of Washington, Seattle.

1997 Graduate Assistant, Curriculum development, Department of Statistics, University of Washington, Seattle

1994–98 Research Assistant, Center for Streamside Studies, School of Fisheries, Quantitative Ecology and Resource Management, and Department of Statistics, University of Washington, Seattle.

TEACHING

2004   Lecturer. Delivered lectures on Bayesian data analysis and the program *structure* at the "Recent Advances in Conservation Genetics" course at the Smithsonian Institution's Conservation & Research Center. August. Front Royal, VA.

2004   Lecturer. Prepared syllabus, wrote lecture notes, and delivered roughly 10 hours of lectures on "Markov chain Monte Carlo for Geneticists" over the course of three days at the Summer Institute for Statistical Genetics. June. Bioinformatics Research Center, North Carolina State University, Raleigh.

1999   Pre-Doctoral Lecturer. Prepared syllabus, delivered all lectures, maintained course web site, wrote exams and problem sets, for the first half of Biology 472, Advanced Undergraduate Ecology. Summer. Department of Biology, University of Washington, Seattle.

1999   Guest Lecturer. Delivered guest lectures on random walks and renewal processes for the undergraduate level stochastic processes course Statistics 396, and a guest lecture on the Monte Carlo method and importance sampling for the graduate-level statistical genetics course, Statistics 578C. Department of Statistics, University of Washington, Seattle.

1997–98   Paid Tutor for students in Statistics 512 and 513 (graduate mathematical statistics), University of Washington.

1995   Teaching Assistant, University of San Francisco Wildlands Study Program. Assisted Dr. John McLaughlin on a three-week summer course studying carnivores and conservation in the North Cascades, Washington.

PUBLICATIONS

ANDERSON, E.C. and Garza, J.C. (2006) The power of single nucleotide polymorphisms for large-scale parentage inference. Genetics 172:2567–2582.

ANDERSON, E.C. (2005) An efficient Monte Carlo method for estimating N_e from temporally-spaced samples using a coalescent-based likelihood. Genetics 170:955–967.

ANDERSON, E.C. and Dunham, K.K. (2005) SPIP 1.0: A program for simulating pedigrees and genetic data in age-structured populations. Molecular Ecology Notes 5:459–461.

Pallsbøll, P. J., Bérube, M., ANDERSON, E.C. and Dunham, K.K (2005). High levels of statistical uncertainty in 'gametic' recapture estimates of male abundance in humpback whales. Marine Ecology Progress Series 295:305–307.

ANDERSON, E.C. and Slatkin, M. (2004) Population genetic basis of haplotype blocks in the 5q31 region. American Journal of Human Genetics 74:40–49.

ANDERSON, E.C. and Novembre, J. (2003) Finding haplotype block boundaries by using the minimum description length criterion. American Journal of Human Genetics 73:336–354.

ANDERSON, E.C. and Slatkin, M. (2003) Orr's quantitative trait loci sign test under conditions of trait ascertainment. Genetics 165:445–446.

ANDERSON, E.C. and Thompson, E.A. (2002) A model-based method for identifying species hybrids using multilocus genetic data. Genetics 160: 1217–1229.

ANDERSON, E.C. and Scheet, P.A. (2001) Improving the estimation of bacterial allele frequencies. Genetics 158: 1383–1386.

ANDERSON, E.C., Williamson, E.G. and Thompson, E.A. (2000)   Monte Carlo evaluation of the likelihood for N_e from temporally-spaced samples. Genetics 156: 2109–2118.

ANDERSON, E.C. and Thompson, E.A. (1999)   MCMC likelihoods for population genetics. Proceedings of the 52nd Session of the International Statistical Institute, 3:347–348.

Naiman, R.J. and ANDERSON, E.C. (1997)   Streams and rivers: their physical and biological variability. In *The Rain Forests of Home: Profile of a North American Bioregion*, ed. P.K. Schoonmaker, B. von Hagen, E.C. Wolf, pp. 131–148. Washington, D.C., Island Press.

THESES AND DISSERTATIONS

ANDERSON, E.C. (2001)   Monte Carlo methods for inference in population genetic models. Ph.D. Dissertation, University of Washington (Advisor: Dr. Elizabeth Thompson).

ANDERSON, E.C. (1998)   Inferring the ancestral origin of sockeye salmon, *Oncorhynchus nerka*, in the Lake Washington basin: A statistical method in theory and application. Master's Thesis. University of Washington (Advisor: Dr. Thomas Sibley).

SOFTWARE AUTHORED

CoNe: Computes the likelihood of N_e given data on two temporally spaced genetic samples using a coalescent based likelihood model.

spip: **S**imulate **P**edigrees **i**n **P**opulations. An application written in C for simulating pedigrees and genetic data in age-structured populations. Described in Anderson and Dunham (2005)

MDBlocks: Minimum Description Length Blocks. An application co-authored in C with John Novembre and distributed for free. It implements the minimum description length model selection procedure and dynamic programming algorithm described in Anderson and Novembre (2003) to delineate haplotype blocks in samples of phased SNP data.

NewHybrids: Program written in C and distributed for free, implementing a Gibbs sampler to estimate the posterior probability that genetically sampled individuals fall into each of a set of user-defined hybrid categories. Described in Anderson, E.C. and Thompson, E.A. (2002).

GF(MC)^2: GLUT for Markov Chain Monte Carlo. A small application programming interface written in C and distributed freely for using the OpenGL Utilities Toolkit to render real-time pictures of Markov Chain Monte Carlo simulations.

MCLEEPS: Monte Carlo Likelihood for Estimation of Effective Population Size. Program written in C and distributed on the World Wide Web for free. Implements the importance sampling algorithm described in Anderson, E.C., Williamson, E.G. and Thompson, E.A. (2000) to estimate a population's genetically effective population size from temporally spaced samples.

SELECTED INVITED TALKS

ANDERSON, E.C. (2006) "Computational and statistical algorithms for parentage inference with single nucleotide polymorphisms" invited to session on Statistical Methods in Computational Biology. Joint Statistical Meetings. Seattle, WA, August.

ANDERSON, E.C. (2003) "Bayesian methods for inferring population structure, hybridization, and migration using multilocus genetic data," invited to the International Workshop on Population Genetics for Animal Conservation, Monte Bondone, Trento, Italy, September.

ANDERSON, E.C. (2001) "Bayesian methods for inference in populations of hybridizing fish," invited to session on Statistics in Fisheries I. Joint meetings of the Statistics Society of Canada, Western North American Region of the International Biometrics Society, and International Mathematics Society. Burnaby, Canada, July.

ANDERSON, E.C. (2000) "Salmon, genetics, and Monte Carlo," invited departmental seminar, Department of Mathematics and Statistics, Simon Fraser University. Burnaby, Canada, April.

SELECTED CONTRIBUTED TALKS

ANDERSON, E.C. (2004) "Efficient Monte Carlo computations on the coalescent for estimating Ne from two temporally-spaced samples," Evolution 2004. Fort Collins, CO. June.

ANDERSON, E.C. (2002) "Identifying species hybrids using multilocus genetic data," Evolution 2002. Urbana-Champaign, June.

ANDERSON, E.C. and Pritchard, J. K. (2000) "Bayesian analysis of population mixture and admixture," International Biometrics Conference, Berkeley, July.

ANDERSON, E.C. (1999) "Analyzing genetic mixtures using reversible jump Markov chain Monte Carlo," informal seminar to the Department of Statistics while visiting the Mathematical Genetics Group, Department of Statistics, University of Oxford, UK, November.

ANDERSON, E.C., Thompson, E.A., and Williamson, E.G. (1999) "Importance sampling for Monte Carlo evaluation of the likelihood for effective population size," Western North American Region of the International Biometrics Society conference, Seattle, June.

ANDERSON, E.C. (1997) "The origins of Lake Washington sockeye salmon: What can genetic data tell us?" presented at the multi-agency Lake Washington Workshop, December.

POSTERS

ANDERSON, E.C. and Novembre, J. (2002) "Haplotype block inference using the minimum description length principle," DIMACS/RECOMB Satellite Workshop on Computational Methods for SNPs and Haplotype Inference, Rutgers University, Piscataway, November 21–22.

REFEREE FOR JOURNALS

American Journal of Human Genetics
Bioinformatics
BioMed Central Bioinformatics
Conservation Genetics
Evolution
Genetical Research
Genetics
Journal of Fish Biology (UK)
Journal of Heredity
Molecular Ecology

Nature Reviews Genetics
North American Journal of Fisheries Management
Theoretical Population Biology